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**Amendments to the Claims:**

This listing of claims will replace all prior versions, and listings of claims in the application:

**Listing of Claims:**

      **1-109.** (canceled)

      **110.** (Currently amended) A method for designing an oligonucleotide sequence having a selected duplex stability comprising:

      a) providing an oligonucleotide having a sequence of N bases and N-1 neighboring base pairs, wherein said oligonucleotide comprises at least one modified base selected from the group consisting of a universal base, unsubstituted and 3-substituted pyrazolo[3,4-d]pyrimidines and 5-substituted pyrimidines; ~~and~~

      b) calculating the duplex stability of said oligonucleotide using an algorithm applying a nearest-neighbor model for duplex formation thermodynamics for each of the N-1 neighboring base pairs, each nearest neighbor thermodynamic parameter defining a thermodynamic contribution of two corresponding neighboring bases, optionally repeating steps a)-b) to obtain a sequence having said selected duplex stability; and

      c) outputting the sequence to a user or a display.

      **111.** (Currently amended) A method for designing an oligonucleotide sequence having a selected duplex stability comprising:

      a) providing an oligonucleotide having a sequence of N bases and N-1 neighboring base pairs, wherein said oligonucleotide comprises at least one modified base selected from the group consisting of a universal base, unsubstituted and 3-substituted pyrazolo[3,4-d]pyrimidines and 5-substituted pyrimidines; and a minor groove binder; ~~and~~

      b) calculating a melting temperature ($T_m$) of said oligonucleotide using an algorithm applying nearest neighbor thermodynamic parameters for each of the N-1 neighboring base pairs, each nearest neighbor thermodynamic parameter defining a thermodynamic

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contribution of two corresponding neighboring bases, optionally repeating steps a)-b) to obtain a sequence having said selected duplex stability; and

> c) outputting the sequence to a user or a display.

**112.** (Previously presented) The method of any one of claims **110** or **111**, wherein said oligonucleotide sequence is derived from a database source.

**113.** (Previously presented) The method of claim **112**, wherein said database source is GENBANK.

**114.** (Previously presented) The method of any one of claims **110** or **111**, wherein said at least one modified base is a member selected from the group consisting of a base attached to an amino acid, a polyamide nucleic acid (PNA) and a locked nucleic acid sugar.

**115.** (Previously presented) The method of claim **114**, wherein said modified base is attached to PNA.

**116.** (Previously presented) The method of claim **114**, wherein said modified base is attached to a locked nucleic acid sugar.

**117.** (Previously presented) The method of any one of claims **110** or **111**, wherein said oligonucleotide has an enhanced ability of mismatch discrimination, in comparison to unmodified nucleotides.

**118.** (Previously presented) The method of any one of claims **110** or **111**, wherein said at least one modified base is a member selected from the group consisting of a universal base, PPA, PPG, PPPA, PPPG, PU, PC, HOPU, HOBuU, HOBuC, $(NH_2)_2PPPA$, $(NH_2)_2PPPAOH$, $(NH_2)_2BuPPAOH$, $(NH_2)_2PPAI$, and HOBuPPG.

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**119.** (Previously presented) The method of claim **110**, wherein said oligonucleotide has attached to it one or more members selected from the group consisting of a minor groove binder, a fluorophore and a quencher.

**120.** (Previously presented) The method of claim **119**, wherein said oligonucleotide sequence has a minor groove binder attached thereto.

**121.** (Previously presented) The method of claim **111** or **120**, wherein said minor groove binder has a formula selected from the group consisting of:
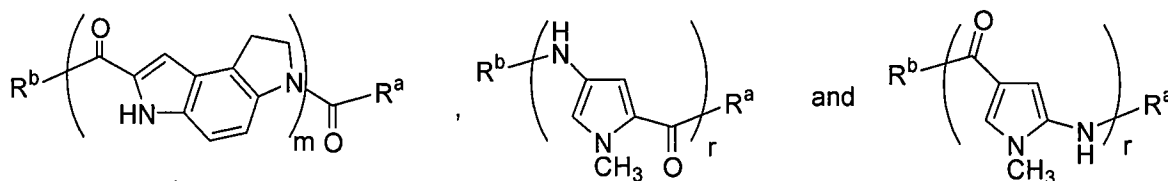


wherein

the subscript m is an integer of from 2 to 5;

the subscript r is an integer of from 2 to 10; and

each $R^a$ and $R^b$ is independently a linking group to said modified oligonucleotide, H, $OR^c$, $NR^cR^d$, $COOR^c$ and $-CONR^cR^d$ wherein each $R^c$ and $R^d$ is selected from the group consisting of H, $(C_1-C_{12})$heteroalkyl, $(C_2-C_{12})$heteroalkenyl, $(C_2-C_{12})$heteroalkynyl, $(C_1-C_{12})$alkyl, $(C_2-C_{12})$alkenyl, $(C_2-C_{12})$alkynyl, aryl$(C_1-C_{12})$alkyl and aryl.

**122.** (Previously presented) The method of claim **120**, wherein said minor groove binder is attached to the oligonucleotide via a quencher molecule.

**123.** (Previously presented) The method of any one of claims **110** or **111**, wherein said algorithm predicts the melting temperature ($T_m$) of said oligonucleotide with an accuracy of about +/- 2°C.

**124.** (Previously presented) The method of any one of claims **110** or **111**, wherein said method is applied to establish conditions for hybridization, renaturation, mapping

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variations of base compositions of sequences or determination of sequence complexity and divergence.

125.    (Previously presented)  The method of any one of claims **110** or **111**, wherein said oligonucleotide is a capture probe in an array.

126.    (Previously presented)  The method of claim **115**, wherein said oligonucleotide an enhanced ability of  mismatch discrimination, in comparison to unmodified nucleotides.

127.    (Previously presented)  The method of claim **116**, wherein said oligonucleotide has an enhanced ability of mismatch discrimination, in comparison to unmodified nucleotides.